

SEQUENCE LISTING

<110> Mahajan, Pramod B.
Shi, Jinrui

<120> A Novel Maize Rad51-Like Gene and Uses
Thereof

<130> 1107

<150> 60/132,582

<151> 1999-05-05

<160> 8

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1474

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (310)...(1192)

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cctaagcgac agcggcggcg tcgacgtaag cggctgcgtg gcgccaccga cggaggctac	180
gagcggttgt ggaggcagat atgagaggtg gaggtggcta caacggggtcg gcggctgtga	240
gatactgaaa tccgcactgc agttctcttc ttcccccaat cagtaccacc tctccaagtg	300
gcaatcacc atg gga gat caa tct ggc tct aga aat gga cca caa cag aag	351
Met Gly Asp Gln Ser Gly Ser Arg Asn Gly Pro Gln Gln Lys	
1 5 10	
tac gtt tca gga gcc cag aat gcc tgg gat atg ttc tct gat gag ctg	399
Tyr Val Ser Gly Ala Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu	
15 20 25 30	
tca cag aaa cac atc act act ggt tct ggt gac ctc aat gac ata ctt	447
Ser Gln Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu	
35 40 45	
ggt ggc ggg att cac tgc aaa gaa gtt act gag atc ggt ggc gtc cca	495
Gly Gly Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro	
50 55 60	
ggg gtt ggt aaa act caa ctg ggg att caa cta gca atc aat gta caa	543
Gly Val Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln	
65 70 75	
atc cca gtg gaa tgt ggt ggc ctt ggt ggg aaa gca gtt tat ata gat	591
Ile Pro Val Glu Cys Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Asp	
80 85 90	
aca gag ggc agt ttc atg gtt gaa cgt gtc tac cag att gct gaa ggg	639
Thr Glu Gly Ser Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly	
95 100 105 110	
tgt att agg gac ata ctg gag cac ttt ccg cac agc cat gag aag tcc	687

Cys	Ile	Arg	Asp	Ile	Leu	Glu	His	Phe	Pro	His	Ser	His	Glu	Lys	Ser		
				115					120					125			
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Ser	Ser	Val	Gln	Lys	Gln	Leu	Gln	Pro	Glu	Arg	Phe	Leu	Ala	Asp	Ile		
			130					135					140				
tat	tac	ttc	cgg	ata	tgc	agt	tac	acc	gaa	caa	att	gca	gtc	ata	aac		783
Tyr	Tyr	Phe	Arg	Ile	Cys	Ser	Tyr	Thr	Glu	Gln	Ile	Ala	Val	Ile	Asn		
		145					150					155					
tac	atg	gag	aag	ttc	ctc	aga	gag	cat	aaa	gat	gtg	cgt	ata	gtt	att		831
Tyr	Met	Glu	Lys	Phe	Leu	Arg	Glu	His	Lys	Asp	Val	Arg	Ile	Val	Ile		
	160					165					170						
att	gat	agt	gtt	act	ttc	cac	ttt	cga	caa	gat	ttt	gaa	gat	ctg	gca		879
Ile	Asp	Ser	Val	Thr	Phe	His	Phe	Arg	Gln	Asp	Phe	Glu	Asp	Leu	Ala		
175					180					185					190		
ctg	agg	acc	aga	gtg	cta	agt	gga	tta	tca	ttg	aag	tta	atg	aag	att		927
Leu	Arg	Thr	Arg	Val	Leu	Ser	Gly	Leu	Ser	Leu	Lys	Leu	Met	Lys	Ile		
			195					200					205				
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Ala	Lys	Thr	Tyr	Asn	Leu	Ala	Val	Val	Leu	Leu	Asn	Gln	Val	Thr	Thr		
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Lys	Phe	Thr	Glu	Gly	Ser	Phe	Gln	Leu	Thr	Leu	Ala	Leu	Gly	Asp	Ser		
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tgg	tcc	cac	tca	tgc	acg	aac	cgg	ttg	att	ctg	cac	tgg	aat	ggg	aac		1071
Trp	Ser	His	Ser	Cys	Thr	Asn	Arg	Leu	Ile	Leu	His	Trp	Asn	Gly	Asn		
	240					245					250						
gaa	cga	tac	gca	cat	ctt	gat	aag	tct	cct	tca	ctt	cca	gta	gcc	tca		1119
Glu	Arg	Tyr	Ala	His	Leu	Asp	Lys	Ser	Pro	Ser	Leu	Pro	Val	Ala	Ser		
255					260					265					270		
gca	ccg	tat	gca	gtg	aca	ggc	aaa	ggg	att	aga	gat	gct	gtg	agc	tca		1167
Ala	Pro	Tyr	Ala	Val	Thr	Gly	Lys	Gly	Ile	Arg	Asp	Ala	Val	Ser	Ser		
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aac	cac	aag	cga	gcc	cga	gta	acg	t	agcattcttg	gtgtcaagca							1212
Asn	His	Lys	Arg	Ala	Arg	Val	Thr										
			290														
ctt	gtat	gtc	cactac	gctc	ctgcag	cttt	cttcgcc	atg	gatctttt	tg	actagt	gagg					1272
tgagact	gga	gaatag	tacc	atttt	gttga	ttctcag	ttg	ctttgtg	ccg	ttggct	acca						1332
accaac	ctta	agagaga	aagt	aaata	caaca	gaacagg	gcta	atatagt	gtt	ttgtat	ctga						1392
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<210> 2
 <211> 294
 <212> PRT
 <213> Zea mays

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 Ser Gly Ala Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu Ser Gln

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<210> 3
<211> 1459
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (169)...(1011)

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gttctcttct tcccccaatc agtaccacct ctccaagtgg caatcacc atg gga gat      177
                                     Met Gly Asp
                                     1

caa tct ggc tct aga aat gga cca caa cag aag tac gtt tca gga gcc      225
Gln Ser Gly Ser Arg Asn Gly Pro Gln Gln Lys Tyr Val Ser Gly Ala
      5                      10                      15

cag aat gcc tgg gat atg ttc tct gat gag ctg tca cag aaa cac atc      273
Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu Ser Gln Lys His Ile
      20                      25                      30                      35

act act ggt tct ggt gac ctc aat gac ata ctt ggt ggc ggg att cac      321
Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly Gly Ile His

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40	45	50	
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caa ctg ggg att caa cta gca atc aat gta caa atc cca gtg gaa tgt Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro Val Glu Cys 70 75 80			417
ggt ggc ctt ggt ggg aaa gca gtt tat ata gag ggc agt ttc atg gtt Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Glu Gly Ser Phe Met Val 85 90 95			465
gaa cgt gtc tac cag att gct gaa ggg tgt att agg gac ata ctg gag Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile Arg Asp Ile Leu Glu 100 105 110 115			513
cac ttt ccg cac agc cat gag aag tcc tct tct gtc caa aaa caa tta His Phe Pro His Ser His Glu Lys Ser Ser Ser Val Gln Lys Gln Leu 120 125 130			561
cag cct gag cgt ttc ctg gcg gat atc tat tac ttc cgg ata tgc agt Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr Phe Arg Ile Cys Ser 135 140 145			609
tac acc gaa caa att gca gtc ata aac tac atg gag aag ttc ctc aga Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met Glu Lys Phe Leu Arg 150 155 160			657
gag cat aaa gat gtg cgt ata gtt att att gat agt gtt act ttc cac Glu His Lys Asp Val Arg Ile Val Ile Ile Asp Ser Val Thr Phe His 165 170 175			705
ttt cga caa gat ttt gaa gat ctg gca ctg agg acc aga gtg cta agt Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg Thr Arg Val Leu Ser 180 185 190 195			753
gga tta tca ttg aag tta atg aag att gca aag aca tat aac ttg gca Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys Thr Tyr Asn Leu Ala 200 205 210			801
gtt gtc ttg ttg aac caa gtc act act aaa ttt aca gaa ggg tca ttt Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe Thr Glu Gly Ser Phe 215 220 225			849
caa ttg act ctt gct cta ggt gac agc tgg tcc cac tca tgc acg aac Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser His Ser Cys Thr Asn 230 235 240			897
cgg ttg att ctg cac tgg aat ggg aac gaa cga tac gca cat ctt gat Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg Tyr Ala His Leu Asp 245 250 255			945
aag tct cct tca ctt cca gta gcc tca gcc ccg tat gca gtg aca ggc Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro Tyr Ala Val Thr Gly 260 265 270 275			993
aaa ggg att aga gat gtg tgagctcaaa ccacaagcga gcccagagtaa Lys Gly Ile Arg Asp Val 280			1041

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tttgtgccgt tggctaccaa ccaaccttaa gagagaagta aatacaacag aacaggctaa 1221
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<211> 281
<212> PRT
<213> Zea mays

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Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly
35     40     45
Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val
50     55     60
Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro
65     70     75     80
Val Glu Cys Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Glu Gly Ser
85     90     95
Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile Arg Asp
100    105    110
Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Ser Val Gln
115    120    125
Lys Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr Phe Arg
130    135    140
Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met Glu Lys
145    150    155    160
Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp Ser Val
165    170    175
Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg Thr Arg
180    185    190
Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys Thr Tyr
195    200    205
Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe Thr Glu
210    215    220
Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser His Ser
225    230    235    240
Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg Tyr Ala
245    250    255
His Leu Asp Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro Tyr Ala
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Val Thr Gly Lys Gly Ile Arg Asp Val
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<210> 5
<211> 1333
<212> DNA
<213> Zea mays

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<220>
<221> CDS
<222> (169)...(1050)

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gttctcttct tcccccaatc agtaccacct ctccaagtgg caatcacc atg gga gat	177
Met Gly Asp	
1	
caa tct ggc tct aga aat gga cca caa cag aag tac gtt tca gga gcc	225
Gln Ser Gly Ser Arg Asn Gly Pro Gln Gln Lys Tyr Val Ser Gly Ala	
5 10 15	
cag aat gcc tgg gat atg ttc tct gat gag ctg tca cag aaa cac atc	273
Gln Asn Ala Trp Asp Met Phe Ser Asp Glu Leu Ser Gln Lys His Ile	
20 25 30 35	
act act ggt tct ggt gac ctc aat gac ata ctt ggt ggc ggg att cac	321
Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly Gly Ile His	
40 45 50	
tgc aaa gaa gtt act gag atc ggt ggc gtc cca ggg gtt ggt aaa act	369
Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val Gly Lys Thr	
55 60 65	
caa ctg ggg att caa cta gca atc aat gta caa atc cca gtg gaa tgt	417
Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro Val Glu Cys	
70 75 80	
ggt ggc ctt ggt ggg aaa gca gtt tat ata gat aca gag ggc agt ttc	465
Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Asp Thr Glu Gly Ser Phe	
85 90 95	
atg gtt gaa cgt gtc tac cag att gct gaa ggg tgt att agg gac ata	513
Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile Arg Asp Ile	
100 105 110 115	
ctg gag cac ttt ccg cac agc cat gag aag tcc tct tct gtc caa aaa	561
Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Ser Val Gln Lys	
120 125 130	
caa tta cag cct gag cgt ttc ctg gcg gat atc tat tac ttc cgg ata	609
Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr Phe Arg Ile	
135 140 145	
tgc agt tac acc gaa caa att gca gtc ata aac tac atg gag aag ttc	657
Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met Glu Lys Phe	
150 155 160	
ctc aga gag cat aaa gat gtg cgt ata gtt att att gat agt gtt act	705
Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp Ser Val Thr	
165 170 175	
ttc cac ttt cga caa gat ttt gaa gat ctg gca ctg agg acc aga gtg	753
Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg Thr Arg Val	
180 185 190 195	
cta agt gga tta tca ttg aag tta atg aag att gca aag aca tat aac	801
Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys Thr Tyr Asn	
200 205 210	
ttg gca gtt gtc ttg ttg aac caa gtc act act aaa ttt aca gaa ggg	849
Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe Thr Glu Gly	
215 220 225	
tca ttt caa ttg act ctt gct cta ggt gac agc tgg tcc cac tca tgc	897

Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser His Ser Cys
 230 235 240

acg aac cgg ttg att ctg cac tgg aat ggg aac gaa cga tac gca cat 945
 Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg Tyr Ala His
 245 250 255

ctt gat aag tct cct tca ctt cca gta gcc tca gca ccg tat gca gtg 993
 Leu Asp Lys Ser Pro Ser Leu Pro Val Ala Ser Ala Pro Tyr Ala Val
 260 265 270 275

aca ggc aaa ggg att aga gat gct gtg agc tca aac cac aag cga gcc 1041
 Thr Gly Lys Gly Ile Arg Asp Ala Val Ser Ser Asn His Lys Arg Ala
 280 285 290

cga gta acg tagcattctt ggtgtcaagc acttgtatgt ccactacgct 1090
 Arg Val Thr

cctgctgctt tcttcgccat ggatcttttg gactagttag gtgagactgg agaatagtag 1150
 cattttgttg attctcagtt gctttgtgcc gttggctacc aaccaacctt aagagagaag 1210
 taaatacaac agaacaggct aatatagtgt tttgtatctg aacatctggs ccatcgtaca 1270
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 aaa 1333

<210> 6
 <211> 294
 <212> PRT
 <213> Zea mays

<400> 6

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 20 25 30

Lys His Ile Thr Thr Gly Ser Gly Asp Leu Asn Asp Ile Leu Gly Gly
 35 40 45

Gly Ile His Cys Lys Glu Val Thr Glu Ile Gly Gly Val Pro Gly Val
 50 55 60

Gly Lys Thr Gln Leu Gly Ile Gln Leu Ala Ile Asn Val Gln Ile Pro
 65 70 75 80

Val Glu Cys Gly Gly Leu Gly Gly Lys Ala Val Tyr Ile Asp Thr Glu
 85 90 95

Gly Ser Phe Met Val Glu Arg Val Tyr Gln Ile Ala Glu Gly Cys Ile
 100 105 110

Arg Asp Ile Leu Glu His Phe Pro His Ser His Glu Lys Ser Ser Ser
 115 120 125

Val Gln Lys Gln Leu Gln Pro Glu Arg Phe Leu Ala Asp Ile Tyr Tyr
 130 135 140

Phe Arg Ile Cys Ser Tyr Thr Glu Gln Ile Ala Val Ile Asn Tyr Met
 145 150 155 160

Glu Lys Phe Leu Arg Glu His Lys Asp Val Arg Ile Val Ile Ile Asp
 165 170 175

Ser Val Thr Phe His Phe Arg Gln Asp Phe Glu Asp Leu Ala Leu Arg
 180 185 190

Thr Arg Val Leu Ser Gly Leu Ser Leu Lys Leu Met Lys Ile Ala Lys
 195 200 205

Thr Tyr Asn Leu Ala Val Val Leu Leu Asn Gln Val Thr Thr Lys Phe
 210 215 220

Thr Glu Gly Ser Phe Gln Leu Thr Leu Ala Leu Gly Asp Ser Trp Ser
 225 230 235 240

His Ser Cys Thr Asn Arg Leu Ile Leu His Trp Asn Gly Asn Glu Arg

	245		250		255										
Tyr	Ala	His	Leu	Asp	Lys	Ser	Pro	Ser	Leu	Pro	Val	Ala	Ser	Ala	Pro
	260		265		270										
Tyr	Ala	Val	Thr	Gly	Lys	Gly	Ile	Arg	Asp	Ala	Val	Ser	Ser	Asn	His
	275		280		285										
Lys	Arg	Ala	Arg	Val	Thr										
290															

<210> 7
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon an adaptor used for cDNA library construction and poly(dT) to remove clones which have a poly(A) tail but no cDNA insert.

<400> 7
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36

<210> 8
 <211> 332
 <212> PRT
 <213> Arabidopsis thaliana

<400> 8

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			20					25					30		
Ile	Arg	Gly	Lys	Leu	Ile	Ser	Ala	Gly	Tyr	Thr	Cys	Leu	Ser	Ser	Ile
		35					40					45			
Ala	Ser	Val	Ser	Ser	Ser	Asp	Leu	Ala	Arg	Ala	Lys	Asn	Ala	Trp	Asp
50						55					60				
Met	Leu	His	Glu	Glu	Glu	Ser	Leu	Pro	Arg	Ile	Thr	Thr	Ser	Cys	Ser
65					70				75					80	
Asp	Leu	Asp	Asn	Ile	Leu	Gly	Gly	Gly	Ile	Ser	Cys	Arg	Asp	Val	Thr
			85					90					95		
Glu	Ile	Gly	Gly	Val	Pro	Gly	Ile	Gly	Lys	Thr	Gln	Ile	Gly	Ile	Gln
		100						105					110		
Leu	Ser	Val	Asn	Val	Gln	Ile	Pro	Arg	Glu	Cys	Gly	Gly	Leu	Gly	Gly
		115					120					125			
Lys	Ala	Ile	Tyr	Ile	Asp	Thr	Glu	Gly	Ser	Phe	Met	Val	Glu	Arg	Ala
130					135					140					
Leu	Gln	Ile	Ala	Glu	Ala	Cys	Val	Glu	Asp	Met	Glu	Glu	Tyr	Thr	Gly
145					150				155						160
Tyr	Met	His	Lys	His	Phe	Gln	Ala	Asn	Gln	Val	Gln	Met	Lys	Pro	Glu
			165					170						175	
Asp	Ile	Leu	Glu	Asn	Ile	Phe	Tyr	Phe	Arg	Val	Cys	Ser	Tyr	Thr	Glu
		180					185						190		
Gln	Ile	Ala	Leu	Val	Asn	His	Leu	Glu	Lys	Phe	Ile	Ser	Glu	Asn	Lys
		195					200					205			
Asp	Val	Val	Val	Ile	Val	Asp	Ser	Ile	Thr	Phe	His	Phe	Arg	Gln	Asp
210					215					220					
Tyr	Asp	Asp	Leu	Ala	Gln	Arg	Thr	Arg	Val	Leu	Ser	Glu	Met	Ala	Leu
225					230					235				240	
Lys	Phe	Met	Lys	Leu	Ala	Lys	Lys	Phe	Ser	Leu	Ala	Val	Val	Leu	Leu
			245					250						255	
Asn	Gln	Val	Thr	Thr	Lys	Phe	Ser	Glu	Gly	Ser	Phe	Gln	Leu	Ala	Leu
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